

A. Mehta
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/156,580A

DATE: 06/17/1999
TIME: 19:03:56

Input Set: I156580A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Takatsuji, Hiroshi
2   Nakagawa, Hitoshi
3   Director General of National Institute of Agrobiological
4   Resources, Ministry of Agriculture, Forestry and Fisheries
5 <120> TITLE OF INVENTION: Method for Shortening Internode of Inflorescence by
6   Introducing Gene for Petunia Transcription Factor PetSPL2
7 <130> FILE REFERENCE: 085761-000400US
8 <140> CURRENT APPLICATION NUMBER: US/09/156,580A
9 <141> CURRENT FILING DATE: 1998-09-18
10 <150> EARLIER APPLICATION NUMBER: JP 10-224852
11 <151> EARLIER FILING DATE: 1998-08-07
12 <160> NUMBER OF SEQ ID NOS: 18
13 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO 1
15 <211> LENGTH: 997
16 <212> TYPE: DNA
17 <213> ORGANISM: Petunia hybrida var. Mitchell
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (190)..(810)
21 <223> OTHER INFORMATION: PetSPL2 transcription factor
22 <400> SEQUENCE: 1
23   cccagtgcc tttttctct ctagtcaagc tctctatc atcatcacta ttcccttggc 60
24   tgcagtaaca ctcctattta accctcacaa aaaaattacc agagggcagc aaaaaatgct 120
25   tgaacataat tattatactt actattaagc tagatttcct cttgatcttg ctagggttga 180
26   ctggagaaa atg gca ggc atg gat aga aac agt ttc aac agt aag tac ttc 231
27   Met Ala Gly Met Asp Arg Asn Ser Phe Asn Ser Lys Tyr Phe
28   1 5 10
29   aaa aac aaa agc atc atg gca aga cag atg gag tac ttg aat aac aac 279
30   Lys Asn Lys Ser Ile Met Ala Arg Gln Met Glu Tyr Leu Asn Asn Asn
31   15 20 25 30
32   aat ggc gac aat aac aac aac aat aat gtt aca agc tca tta cga gat 327
33   Asn Gly Asp Asn Asn Asn Asn Asn Val Thr Ser Ser Leu Arg Asp
34   35 40 45
35   aat tat gga aat gaa gat cat tta ctt ggt gga cta ttc tct tgg cct 375
36   Asn Tyr Gly Asn Glu Asp His Leu Leu Gly Gly Leu Phe Ser Trp Pro
37   50 55 60
38   cca aga tct tat aca tgt agc ttt tgt aaa agg gaa ttt aga tct gct 423
39   Pro Arg Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala
40   65 70 75
41   caa gct ctt ggt gga cac atg aat gtt cat aga aga gat aga gcc att 471
42   Gln Ala Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Ile
43   80 85 90
44   ttg aga caa tca cca cct aga gat att aat agg tat tct ctt cta aac 519
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45      Leu Arg Gln Ser Pro Pro Arg Asp Ile Asn Arg Tyr Ser Leu Leu Asn
46      95                      100                      105                      110
47      ctt aat ctt gaa cca aac cct aac ttt tac cct agt cat aac cct agt 567
48      Leu Asn Leu Glu Pro Asn Pro Asn Phe Tyr Pro Ser His Asn Pro Ser
49                      115                      120                      125
50      ttt tca aga aaa ttc cca cct ttt gaa atg agg aaa tta gga aaa gga 615
51      Phe Ser Arg Lys Phe Pro Pro Phe Glu Met Arg Lys Leu Gly Lys Gly
52                      130                      135                      140
53      gtt gtt cca aac aat cac ttg aaa agt gcc aga ggg cgt ttt gga gtt 663
54      Val Val Pro Asn Asn His Leu Lys Ser Ala Arg Gly Arg Phe Gly Val
55                      145                      150                      155
56      gag aaa att gac tct ttc atg caa gaa aaa gaa tgt act act aca gtg 711
57      Glu Lys Ile Asp Ser Phe Met Gln Glu Lys Glu Cys Thr Thr Thr Val
58                      160                      165                      170
59      atc aag aag tcc gag ttt cta aga ttg gac ttg gga att ggg ttg atc 759
60      Ile Lys Lys Ser Glu Phe Leu Arg Leu Asp Leu Gly Ile Gly Leu Ile
61      175                      180                      185                      190
62      agt gaa tca aag gaa gat tta gat ctt gaa ctt cga ctg gga tcc act 807
63      Ser Glu Ser Lys Glu Asp Leu Asp Leu Glu Leu Arg Leu Gly Ser Thr
64                      195                      200                      205
65      taactatatc taattttttac ggcattaagg tttgttaaatt gagtcgacag cttagtcaaa 867
66      actacttatg cactttaata tggtttcttg tgctatatatt atttatttta catggctgta 927
67      tctaggtttg cattttaaga ttttagtacct tgtcagatta aaagaaaacg aaagttaaatt 987
68      taaaaaaaaa 997
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70      <211> LENGTH: 206
71      <212> TYPE: PRT
72      <213> ORGANISM: Petunia sp.
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74      Met Ala Gly Met Asp Arg Asn Ser Phe Asn Ser Lys Tyr Phe Lys Asn
75      1                      5                      10                      15
76      Lys Ser Ile Met Ala Arg Gln Met Glu Tyr Leu Asn Asn Asn Asn Gly
77      20                      25                      30
78      Asp Asn Asn Asn Asn Asn Asn Val Thr Ser Ser Leu Arg Asp Asn Tyr
79      35                      40                      45
80      Gly Asn Glu Asp His Leu Leu Gly Gly Leu Phe Ser Trp Pro Pro Arg
81      50                      55                      60
82      Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala
83      65                      70                      75                      80
84      Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Ile Leu Arg
85      85                      90                      95
86      Gln Ser Pro Pro Arg Asp Ile Asn Arg Tyr Ser Leu Leu Asn Leu Asn
87      100                      105                      110
88      Leu Glu Pro Asn Pro Asn Phe Tyr Pro Ser His Asn Pro Ser Phe Ser
89      115                      120                      125
90      Arg Lys Phe Pro Pro Phe Glu Met Arg Lys Leu Gly Lys Gly Val Val
91      130                      135                      140
92      Pro Asn Asn His Leu Lys Ser Ala Arg Gly Arg Phe Gly Val Glu Lys
93      145                      150                      155                      160
94      Ile Asp Ser Phe Met Gln Glu Lys Glu Cys Thr Thr Thr Val Ile Lys

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95             165             170             175
96      Lys Ser Glu Phe Leu Arg Leu Asp Leu Gly Ile Gly Leu Ile Ser Glu
97             180             185             190
98      Ser Lys Glu Asp Leu Asp Leu Glu Leu Arg Leu Gly Ser Thr
99             195             200             205

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105 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
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107 <220> FEATURE:
108 <221> NAME/KEY: modified_base
109 <222> LOCATION: (6)
110 <223> OTHER INFORMATION: i
111 <220> FEATURE:
112 <221> NAME/KEY: modified_base
113 <222> LOCATION: (9)
114 <223> OTHER INFORMATION: i
115 <220> FEATURE:
116 <221> NAME/KEY: modified_base
117 <222> LOCATION: (12)
118 <223> OTHER INFORMATION: i
119 <220> FEATURE:
120 <221> NAME/KEY: modified_base
121 <222> LOCATION: (15)
122 <223> OTHER INFORMATION: i
123 <400> SEQUENCE: 3
w--> 124      c a r g c n y t n g g n g g n c a y
125 <210> SEQ ID NO 4
126 <211> LENGTH: 18
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
131     primer 2
132 <220> FEATURE:
133 <221> NAME/KEY: modified_base
134 <222> LOCATION: (3)
135 <223> OTHER INFORMATION: i
136 <220> FEATURE:
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138 <222> LOCATION: (6)
139 <223> OTHER INFORMATION: i
140 <220> FEATURE:
141 <221> NAME/KEY: modified_base
142 <222> LOCATION: (9)
143 <223> OTHER INFORMATION: i
144 <400> SEQUENCE: 4

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 147 <211> LENGTH: 17
 148 <212> TYPE: DNA
 149 <213> ORGANISM: Artificial Sequence
 150 <220> FEATURE:
 151 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
 152 primer 3
 153 <220> FEATURE:
 154 <221> NAME/KEY: modified_base
 155 <222> LOCATION: (3)
 156 <223> OTHER INFORMATION: i
 157 <220> FEATURE:
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 159 <222> LOCATION: (6)
 160 <223> OTHER INFORMATION: i
 161 <220> FEATURE:
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 163 <222> LOCATION: (12)
 164 <223> OTHER INFORMATION: i
 w-->OK 165 <400> SEQUENCE: 5
 166 arncknaryt cnarrtc 17
 167 <210> SEQ ID NO 6
 168 <211> LENGTH: 6
 169 <212> TYPE: PRT
 170 <213> ORGANISM: Artificial Sequence
 171 <220> FEATURE:
 172 <223> OTHER INFORMATION: Description of Artificial Sequence:amino acids
 173 present in both SUPERMAN gene of Arabidopsis
 174 thaliana and GmN479 gene of soy bean root nodules
 175 <400> SEQUENCE: 6
 176 Gln Ala Leu Gly Gly His
 177 1 5
 178 <210> SEQ ID NO 7
 179 <211> LENGTH: 6
 180 <212> TYPE: PRT
 181 <213> ORGANISM: Artificial Sequence
 182 <220> FEATURE:
 183 <223> OTHER INFORMATION: Description of Artificial Sequence:amino acids
 184 present in both SUPERMAN gene of Arabidopsis
 185 thaliana and GmN479 gene of soy bean root nodules
 186 <400> SEQUENCE: 7
 187 Leu Gly Gly His Met Asn
 188 1 5
 189 <210> SEQ ID NO 8
 190 <211> LENGTH: 6
 191 <212> TYPE: PRT
 192 <213> ORGANISM: Artificial Sequence
 193 <220> FEATURE:
 194 <223> OTHER INFORMATION: Description of Artificial Sequence:amino acids

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195      present in both SUPERMAN gene of Arabidopsis
196      thaliana and GmN479 gene of soy bean root nodules
197  <400> SEQUENCE: 8
198      Asp Leu Glu Leu Arg Leu
199          1              5
200  <210> SEQ ID NO 9
201  <211> LENGTH: 43
202  <212> TYPE: PRT
203  <213> ORGANISM: Artificial Sequence
204  <220> FEATURE:
205  <223> OTHER INFORMATION: Description of Artificial Sequence: SUPERMAN zinc
206      finger motif
207  <400> SEQUENCE: 9
208      Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala
209          1              5              10              15
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211          20              25              30
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213          35              40
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215  <211> LENGTH: 42
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218  <220> FEATURE:
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223          1              5              10              15
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225          20              25              30
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227          35              40
228  <210> SEQ ID NO 11
229  <211> LENGTH: 41
230  <212> TYPE: PRT
231  <213> ORGANISM: Artificial Sequence
232  <220> FEATURE:
233  <223> OTHER INFORMATION: Description of Artificial Sequence: PetSPL2 zinc
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235  <400> SEQUENCE: 11
236      Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala
237          1              5              10              15
238      Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Ile Leu Arg
239          20              25              30
240      Gln Ser Pro Pro Arg Asp Ile Asn Arg
241          35              40
242  <210> SEQ ID NO 12
243  <211> LENGTH: 43
244  <212> TYPE: PRT

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

124 W "N" or "Xaa" used: Feature required

cargcnytn gnggncay

145 W "N" or "Xaa" used: Feature required

ytnggnggnc ayatgaay

166 W "N" or "Xaa" used: Feature required

arncknaryt cnarrtc